STIC-Biotech/ChemLib 180695

From: JEFFREY RUSSEL [jeffrey.russel@uspto.gov]
Sent: Monday, February 27, 2006 4:38 PM
To: STIC-Biotech/ChemLib
Subject: Database Search Request, Serial Number: 10/649,378

Requester:
JEFFREY RUSSEL (P/1654)
Art Unit:
GROUP ART UNIT 1654
Employee Number:
62785
Office Location:
REM 03D19
Phone Number:
(571)272-0969
Mailbox Number:
REM 3C18

Case serial number:
10/649,378
Class / Subclass(es):
NA
Earliest Priority Filing Date:
NA
Format preferred for results:
Diskette
Search Topic Information:
Please do an interference search of SEQ ID NO:250 in the U.S. patent application sequence database (pending, published, and issued). Please require any hits to have ten or fewer residues. Thank you.
Special Instructions and Other Comments:

FEB 27 2006 (STIC)

********** Point of Contact
Searcher:_____ Alexandra Waclawiw
Searcher Phone:_____ Technical Info Specia
Date Searcher Picked up:3-2
Date completed:_____ 3-2
Searcher Prep Time:_8_
Online Time:_____6

****
Type of Search
NA#_____ AA#:_1_
S/L:_____ Oligomer:_____
Encode/Transl:_____
Structure #:_____Text:____
Inventor:_____ Litigation:___

****
Vendors and cost where applicable
STN:_____
DIALOG:_____
QUESTEL/ORBIT:_____
LEXIS/NEXIS:_____
SEQUENCE SYSTEM:_____
WWW/Internet:_____
Other (Specify):_____

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 2, 2006, 12:36:46 ; Search time 36 Seconds
(without alignments)
8.578 Million cell updates/sec

Title: US-10-649-378B-250
Perfect score: 20
Sequence: 1 FREL 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 322452 seqs, 77201678 residues

Total number of hits satisfying chosen parameters: 38129

Minimum DB seq length: 0
Maximum DB seq length: 11

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : Pending_Patents_AA_New:*
1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*
2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/ptodata/2/paa/US11_NEW_COMB.pep:*
8: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*

Search completed: March 2, 2006, 12:46:38
Job time : 37 secs

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 2, 2006, 12:36:36 ; Search time 552 Seconds
(without alignments)
10.014 Million cell updates/sec

Title: US-10-649-378B-250
Perfect score: 20
Sequence: 1 FREL 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 7861189 seqs, 1381955077 residues

Total number of hits satisfying chosen parameters: 941471

Minimum DB seq length: 0
Maximum DB seq length: 11

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : Pending_Patents_AA_Main:*
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44: /cgn2_6/ptodata/1/paa/US600_COMB.pep:*
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49: /cgn2_6/ptodata/1/paa/US605_COMB.pep:*
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51: /cgn2_6/ptodata/1/paa/US607_COMB.pep:*

Search completed: March 2, 2006, 12:45:58
Job time : 554 secs

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 2, 2006, 12:46:51 ; Search time 20 Seconds
(without alignments)
4.000 Million cell updates/sec

Title: US-10-649-378B-250
Perfect score: 20
Sequence: 1 FREL 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 135339 seqs, 20000136 residues

Total number of hits satisfying chosen parameters: 49350

Minimum DB seq length: 0
Maximum DB seq length: 11

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : Published_Applications_AA_New:*
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	20	100.0	8	7	US-11-045-024-1624	Sequence 1624, Ap
2	20	100.0	8	7	US-11-045-024-4338	Sequence 4338, Ap
3	20	100.0	8	7	US-11-045-024-10299	Sequence 10299, A
4	20	100.0	8	7	US-11-045-024-10329	Sequence 10329, A
5	20	100.0	8	7	US-11-045-024-12138	Sequence 12138, A
6	20	100.0	8	7	US-11-045-024-12157	Sequence 12157, A
7	20	100.0	9	7	US-11-045-024-3221	Sequence 3221, Ap
8	20	100.0	9	7	US-11-045-024-5832	Sequence 5832, Ap
9	20	100.0	9	7	US-11-045-024-10302	Sequence 10302, A

10	20	100.0	9	7	US-11-045-024-10338	Sequence 10338, A
11	20	100.0	9	7	US-11-045-024-12141	Sequence 12141, A
12	20	100.0	9	7	US-11-045-024-12164	Sequence 12164, A
13	20	100.0	9	7	US-11-045-024-13786	Sequence 13786, A
14	20	100.0	10	7	US-11-045-024-3292	Sequence 3292, Ap
15	20	100.0	10	7	US-11-045-024-3293	Sequence 3293, Ap
16	20	100.0	10	7	US-11-045-024-5877	Sequence 5877, Ap
17	20	100.0	10	7	US-11-045-024-10310	Sequence 10310, A
18	20	100.0	10	7	US-11-045-024-10341	Sequence 10341, A
19	20	100.0	10	7	US-11-045-024-12146	Sequence 12146, A
20	20	100.0	10	7	US-11-045-024-12168	Sequence 12168, A
21	20	100.0	11	7	US-11-045-024-2286	Sequence 2286, Ap
22	20	100.0	11	7	US-11-045-024-3374	Sequence 3374, Ap
23	20	100.0	11	7	US-11-045-024-4753	Sequence 4753, Ap
24	20	100.0	11	7	US-11-045-024-5946	Sequence 5946, Ap
25	20	100.0	11	7	US-11-045-024-10314	Sequence 10314, A
26	20	100.0	11	7	US-11-045-024-12150	Sequence 12150, A
27	20	100.0	11	7	US-11-045-024-12799	Sequence 12799, A
28	17	85.0	9	6	US-10-510-101-123	Sequence 123, App
29	16	80.0	5	6	US-10-516-083-8	Sequence 8, Appli
30	16	80.0	6	6	US-10-485-788A-233	Sequence 233, App
31	16	80.0	7	6	US-10-485-788A-234	Sequence 234, App
32	16	80.0	8	6	US-10-485-788A-235	Sequence 235, App
33	16	80.0	8	7	US-11-058-735-21	Sequence 21, Appl
34	16	80.0	8	7	US-11-045-024-4306	Sequence 4306, Ap
35	16	80.0	8	7	US-11-045-024-4307	Sequence 4307, Ap
36	16	80.0	8	7	US-11-045-024-9685	Sequence 9685, Ap
37	16	80.0	8	7	US-11-045-024-10058	Sequence 10058, A
38	16	80.0	8	7	US-11-045-024-12706	Sequence 12706, A
39	16	80.0	8	7	US-11-045-024-12764	Sequence 12764, A
40	15	75.0	4	6	US-10-895-064-963	Sequence 963, App
41	15	75.0	4	7	US-11-129-741-963	Sequence 963, App
42	15	75.0	5	6	US-10-925-366A-61	Sequence 61, Appl
43	15	75.0	8	6	US-10-895-064-1143	Sequence 1143, Ap
44	15	75.0	8	7	US-11-123-290-6	Sequence 6, Appli
45	15	75.0	8	7	US-11-123-290-46	Sequence 46, Appl
46	15	75.0	8	7	US-11-123-290-55	Sequence 55, Appl
47	15	75.0	8	7	US-11-066-967-2	Sequence 2, Appli
48	15	75.0	8	7	US-11-066-967-19	Sequence 19, Appl
49	15	75.0	8	7	US-11-129-741-1143	Sequence 1143, Ap
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52	15	75.0	9	7	US-11-129-741-4218	Sequence 4218, Ap
53	15	75.0	10	7	US-11-058-727-111	Sequence 111, App
54	15	75.0	10	7	US-11-108-389-111	Sequence 111, App
55	15	75.0	10	7	US-11-123-290-62	Sequence 62, Appl
56	15	75.0	10	7	US-11-123-290-68	Sequence 68, Appl
57	15	75.0	10	7	US-11-123-290-73	Sequence 73, Appl
58	15	75.0	10	7	US-11-224-624-111	Sequence 111, App
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60	15	75.0	11	7	US-11-123-290-69	Sequence 69, Appl
61	15	75.0	11	7	US-11-123-290-74	Sequence 74, Appl
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63	14	70.0	7	7	US-11-129-741-1431	Sequence 1431, Ap
64	14	70.0	8	7	US-11-045-024-114	Sequence 114, App
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88	14	70.0	8	7	US-11-045-024-11408	Sequence 11408, A
89	14	70.0	8	7	US-11-033-039-387	Sequence 387, App
90	14	70.0	8	7	US-11-041-893-156	Sequence 156, App
91	14	70.0	8	7	US-11-131-425A-84	Sequence 84, Appl
92	14	70.0	9	6	US-10-981-873-17	Sequence 17, Appl
93	14	70.0	9	6	US-10-859-643-372	Sequence 372, App
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95	14	70.0	9	6	US-10-895-064-1363	Sequence 1363, Ap
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128	14	70.0	9	7	US-11-045-024-11449	Sequence 11449, A
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131	14	70.0	9	7	US-11-045-024-13670	Sequence 13670, A
132	14	70.0	9	7	US-11-045-024-14150	Sequence 14150, A
133	14	70.0	9	7	US-11-033-039-827	Sequence 827, App
134	14	70.0	9	7	US-11-233-796-3	Sequence 3, Appli
135	14	70.0	9	7	US-11-116-203-61	Sequence 61, Appl
136	14	70.0	9	7	US-11-116-203-62	Sequence 62, Appl
137	14	70.0	9	7	US-11-018-868-98	Sequence 98, Appl
138	14	70.0	9	7	US-11-018-868-109	Sequence 109, App
139	14	70.0	9	7	US-11-129-741-1363	Sequence 1363, Ap
140	14	70.0	9	7	US-11-222-745-19	Sequence 19, Appl
141	14	70.0	10	6	US-10-859-643-73	Sequence 73, Appl
142	14	70.0	10	6	US-10-859-643-506	Sequence 506, App
143	14	70.0	10	6	US-10-859-643-603	Sequence 603, App
144	14	70.0	10	6	US-10-989-767A-414	Sequence 414, App
145	14	70.0	10	6	US-10-989-767A-543	Sequence 543, App
146	14	70.0	10	7	US-11-097-864-73	Sequence 73, Appl
147	14	70.0	10	7	US-11-097-864-506	Sequence 506, App
148	14	70.0	10	7	US-11-097-864-603	Sequence 603, App
149	14	70.0	10	7	US-11-097-912-73	Sequence 73, Appl
150	14	70.0	10	7	US-11-097-912-506	Sequence 506, App

ALIGNMENTS

RESULT 1
US-11-045-024-1624
; Sequence 1624, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney,John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205

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;  PRIOR FILING DATE: 1993-06-04
;  PRIOR APPLICATION NUMBER: US 08/103,396
;  PRIOR FILING DATE: 1993-08-06
;  PRIOR APPLICATION NUMBER: US 08/159,184
;  PRIOR FILING DATE: 1993-11-29
;  PRIOR APPLICATION NUMBER: US 08/159,339
;  PRIOR FILING DATE: 1993-11-29
;  PRIOR APPLICATION NUMBER: US 08/205,713
;  PRIOR FILING DATE: 1994-03-04
;  PRIOR APPLICATION NUMBER: US 08/347,610
;  PRIOR FILING DATE: 1994-12-01
;  NUMBER OF SEQ ID NOS: 14528
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1624
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-1624

  Query Match             100.0%;  Score 20;  DB 7;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 9.9e+04;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FREL 4
              ||||
Db          5 FREL 8



RESULT 28
US-10-510-101-123
; Sequence 123, Application US/10510101
; Publication No. US20060018915A1
; GENERAL INFORMATION:
;  APPLICANT: Epimmune Inc.
;  APPLICANT:  Ishioka, Glenn
;  APPLICANT:  Fikes, John
;  APPLICANT:  Tangri, Shabnam
;  APPLICANT:  Sette, Alessandro
;  TITLE OF INVENTION: Heteroclitic Analogs and Related Methods
;  FILE REFERENCE: 2060.009PC05
;  CURRENT APPLICATION NUMBER: US/10/510,101
;  CURRENT FILING DATE:  2004-10-05
;  PRIOR APPLICATION NUMBER: US 60/413,471
;  PRIOR FILING DATE: 2002-09-26
;  PRIOR APPLICATION NUMBER: US 10/116,118
;  PRIOR FILING DATE: 2002-04-05
;  NUMBER OF SEQ ID NOS: 196
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 123
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic peptide derived from Homo sapiens Her2/neu
US-10-510-101-123
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Query Match 85.0%; Score 17; DB 6; Length 9;
Best Local Similarity 75.0%; Pred. No. 9.9e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db          2 YREL 5
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Search completed: March 2, 2006, 12:49:52
Job time : 21 secs

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 2, 2006, 12:46:16 ; Search time 161 Seconds
(without alignments)
10.381 Million cell updates/sec

Title: US-10-649-378B-250
Perfect score: 20
Sequence: 1 FREL 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 251271

Minimum DB seq length: 0
Maximum DB seq length: 11

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : Published_Applications_AA_Main:*
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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	20	100.0	4	5	US-10-649-378A-250	Sequence 250, App
2	20	100.0	4	5	US-10-649-378A-337	Sequence 337, App
3	20	100.0	7	4	US-10-001-546-43	Sequence 43, Appl
4	20	100.0	8	3	US-09-797-410-5	Sequence 5, Appli
5	20	100.0	8	3	US-09-017-743C-98	Sequence 98, Appl
6	20	100.0	8	4	US-10-117-937-349	Sequence 349, App
7	20	100.0	8	4	US-10-149-138-1566	Sequence 1566, Ap
8	20	100.0	8	4	US-10-149-138-1616	Sequence 1616, Ap
9	20	100.0	8	4	US-10-149-138-1627	Sequence 1627, Ap
10	20	100.0	8	4	US-10-149-138-2282	Sequence 2282, Ap
11	20	100.0	8	4	US-10-182-252A-1315	Sequence 1315, Ap

12	20	100.0	8	4	US-10-182-252A-1347	Sequence 1347, Ap
13	20	100.0	8	4	US-10-362-263-5	Sequence 5, Appli
14	20	100.0	8	4	US-10-149-138-1566	Sequence 1566, Ap
15	20	100.0	8	4	US-10-149-138-1616	Sequence 1616, Ap
16	20	100.0	8	4	US-10-149-138-1627	Sequence 1627, Ap
17	20	100.0	8	4	US-10-149-138-2282	Sequence 2282, Ap
18	20	100.0	8	6	US-11-067-064-349	Sequence 349, App
19	20	100.0	8	6	US-11-051-411-331	Sequence 331, App
20	20	100.0	8	6	US-11-051-411-430	Sequence 430, App
21	20	100.0	8	6	US-11-051-411-748	Sequence 748, App
22	20	100.0	8	6	US-11-051-411-1049	Sequence 1049, Ap
23	20	100.0	8	6	US-11-067-159-349	Sequence 349, App
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25	20	100.0	9	3	US-09-277-064-35	Sequence 35, Appl
26	20	100.0	9	4	US-10-001-546-42	Sequence 42, Appl
27	20	100.0	9	4	US-10-133-210-48	Sequence 48, Appl
28	20	100.0	9	4	US-10-133-210-82	Sequence 82, Appl
29	20	100.0	9	4	US-10-133-210-122	Sequence 122, App
30	20	100.0	9	4	US-10-239-313A-116	Sequence 116, App
31	20	100.0	9	4	US-10-200-708-667	Sequence 667, App
32	20	100.0	9	4	US-10-117-937-350	Sequence 350, App
33	20	100.0	9	4	US-10-117-937-351	Sequence 351, App
34	20	100.0	9	4	US-10-117-937-353	Sequence 353, App
35	20	100.0	9	4	US-10-442-909-58	Sequence 58, Appl
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44	20	100.0	9	4	US-10-149-138-4102	Sequence 4102, Ap
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54	20	100.0	9	6	US-11-067-159-350	Sequence 350, App
55	20	100.0	9	6	US-11-067-159-351	Sequence 351, App
56	20	100.0	9	6	US-11-067-159-353	Sequence 353, App
57	20	100.0	10	3	US-09-229-173-43	Sequence 43, Appl
58	20	100.0	10	4	US-10-001-546-41	Sequence 41, Appl
59	20	100.0	10	4	US-10-200-708-48	Sequence 48, Appl
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61	20	100.0	10	4	US-10-200-708-98	Sequence 98, Appl
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63	20	100.0	10	4	US-10-200-708-149	Sequence 149, App
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65	20	100.0	10	4	US-10-200-708-198	Sequence 198, App
66	20	100.0	10	4	US-10-200-708-668	Sequence 668, App
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74	20	100.0	10	6	US-11-051-411-280	Sequence 280, App
75	20	100.0	10	6	US-11-051-411-431	Sequence 431, App
76	20	100.0	10	6	US-11-051-411-1039	Sequence 1039, Ap
77	20	100.0	10	6	US-11-067-159-352	Sequence 352, App
78	20	100.0	11	4	US-10-442-909-60	Sequence 60, Appl
79	20	100.0	11	4	US-10-442-909-61	Sequence 61, Appl
80	20	100.0	11	4	US-10-149-138-1567	Sequence 1567, Ap
81	20	100.0	11	4	US-10-149-138-1628	Sequence 1628, Ap
82	20	100.0	11	4	US-10-149-138-1770	Sequence 1770, Ap
83	20	100.0	11	4	US-10-149-138-2283	Sequence 2283, Ap
84	20	100.0	11	4	US-10-149-138-3000	Sequence 3000, Ap
85	20	100.0	11	4	US-10-149-138-3532	Sequence 3532, Ap
86	20	100.0	11	4	US-10-149-138-4620	Sequence 4620, Ap
87	20	100.0	11	4	US-10-149-138-1567	Sequence 1567, Ap
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95	20	100.0	11	6	US-11-051-411-435	Sequence 435, App
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114	17	85.0	8	4	US-10-837-217-783	Sequence 783, App
115	17	85.0	9	3	US-09-909-460-103	Sequence 103, App
116	17	85.0	9	3	US-09-872-836-103	Sequence 103, App
117	17	85.0	9	4	US-10-015-535-37	Sequence 37, Appl
118	17	85.0	9	4	US-10-128-711-67	Sequence 67, Appl
119	17	85.0	9	4	US-10-133-210-281	Sequence 281, App
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121	17	85.0	9	4	US-10-154-884B-10963	Sequence 10963, A
122	17	85.0	9	4	US-10-149-138-4323	Sequence 4323, Ap
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133	17	85.0	9	4	US-10-837-217-397	Sequence 397, App
134	17	85.0	9	4	US-10-764-390-236	Sequence 236, App
135	17	85.0	9	5	US-10-758-970-103	Sequence 103, App
136	17	85.0	9	5	US-10-705-459-262	Sequence 262, App
137	17	85.0	9	5	US-10-888-348-47	Sequence 47, Appl
138	17	85.0	9	5	US-10-888-348-48	Sequence 48, Appl
139	17	85.0	9	5	US-10-888-348-87	Sequence 87, Appl
140	17	85.0	9	5	US-10-888-348-161	Sequence 161, App
141	17	85.0	9	5	US-10-888-348-164	Sequence 164, App
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147	17	85.0	9	5	US-10-820-067A-101	Sequence 101, App
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149	17	85.0	10	4	US-10-794-899-87	Sequence 87, Appl
150	17	85.0	10	5	US-10-478-451-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1
US-10-649-378A-250
; Sequence 250, Application US/10649378A
; Publication No. US20040254120A1
; GENERAL INFORMATION:
; APPLICANT: FOGELMAN, ALAN M.
; APPLICANT: ANANTHARAMAIAH, GATTADAHALLI M.
; APPLICANT: NAVAB, MOHAMAD
; TITLE OF INVENTION: ORALLY ADMINISTERED SMALL PEPTIDES SYNERGIZE STATIN ACTIVITY
; FILE REFERENCE: 407T-911270US
; CURRENT APPLICATION NUMBER: US/10/649,378A
; CURRENT FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: US10/423,830
; PRIOR FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: US10/273,386
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US10/187,215
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US09/896,841
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US09/645,454
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US60/494,449
; PRIOR FILING DATE: 2003-08-11
; NUMBER OF SEQ ID NOS: 464
; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 250
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically synthesized peptide. Amino acids can be protected or
; OTHER INFORMATION: unprotected D or L form.
US-10-649-378A-250

Query Match 100.0%; Score 20; DB 5; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 FREL 4
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RESULT 3
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; Sequence 43, Application US/10001546
; Publication No. US20030027766A1
; GENERAL INFORMATION:
; APPLICANT: IOANNIDES, CONSTANTIN G.
; APPLICANT: FISK, BRYAN A.
; APPLICANT: IOANNIDES, MARIA G.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STIMULATING
; TITLE OF INVENTION: T-LYMPHOCYTES
; FILE REFERENCE: UTSC:390USC2
; CURRENT APPLICATION NUMBER: US/10/001,546
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 08/403,459
; PRIOR FILING DATE: 1995-03-14
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-001-546-43

Query Match 100.0%; Score 20; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 FREL 4
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Db          2 FREL 5
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Search completed: March 2, 2006, 12:49:26
Job time : 163 secs

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 2, 2006, 12:35:11 ; Search time 23 Seconds
(without alignments)
14.378 Million cell updates/sec

Title: US-10-649-378B-250
Perfect score: 20
Sequence: 1 FREL 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 143663

Minimum DB seq length: 0
Maximum DB seq length: 11

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

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4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	20	100.0	7	2	US-08-403-459-43	Sequence 43, Appl
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3	20	100.0	8	1	US-08-458-218-21	Sequence 21, Appl
4	20	100.0	8	1	US-08-450-497-21	Sequence 21, Appl
5	20	100.0	8	2	US-08-450-482B-21	Sequence 21, Appl
6	20	100.0	8	2	US-08-151-064D-21	Sequence 21, Appl
7	20	100.0	9	1	US-08-338-634-25	Sequence 25, Appl
8	20	100.0	9	2	US-08-159-339A-540	Sequence 540, App
9	20	100.0	9	2	US-08-403-459-42	Sequence 42, Appl
10	20	100.0	9	4	PCT-US95-16415-35	Sequence 35, Appl
11	20	100.0	10	1	US-08-537-400-33	Sequence 33, Appl

12	20	100.0	10	2	US-08-159-339A-547	Sequence 547, App
13	20	100.0	10	2	US-08-403-459-41	Sequence 41, Appl
14	18	90.0	7	1	US-08-962-284-11	Sequence 11, Appl
15	18	90.0	9	2	US-09-148-545-273	Sequence 273, App
16	18	90.0	9	2	US-09-621-011-273	Sequence 273, App
17	18	90.0	10	2	US-09-211-715-197	Sequence 197, App
18	17	85.0	7	1	US-08-719-758-19	Sequence 19, Appl
19	17	85.0	7	2	US-09-119-827-19	Sequence 19, Appl
20	17	85.0	8	2	US-09-177-249-104	Sequence 104, App
21	17	85.0	8	2	US-08-817-832B-27	Sequence 27, Appl
22	17	85.0	8	2	US-09-812-283-104	Sequence 104, App
23	17	85.0	9	1	US-08-787-547-103	Sequence 103, App
24	17	85.0	9	2	US-08-159-339A-246	Sequence 246, App
25	17	85.0	9	2	US-08-159-339A-564	Sequence 564, App
26	17	85.0	9	2	US-08-464-496-9	Sequence 9, Appli
27	17	85.0	9	2	US-08-197-484-67	Sequence 67, Appl
28	17	85.0	9	2	US-09-743-467-1	Sequence 1, Appli
29	17	85.0	9	4	PCT-US92-07218-9	Sequence 9, Appli
30	17	85.0	9	4	PCT-US95-02121-67	Sequence 67, Appl
31	17	85.0	10	2	US-08-840-006-3	Sequence 3, Appli
32	17	85.0	10	2	US-08-464-496-6	Sequence 6, Appli
33	17	85.0	10	2	US-09-239-043D-2481	Sequence 2481, Ap
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35	17	85.0	10	4	PCT-US92-07218-6	Sequence 6, Appli
36	16	80.0	4	1	US-08-685-589A-2	Sequence 2, Appli
37	16	80.0	5	1	US-08-122-792-2	Sequence 2, Appli
38	16	80.0	5	1	US-08-121-713D-14	Sequence 14, Appl
39	16	80.0	5	1	US-08-835-268-14	Sequence 14, Appl
40	16	80.0	5	1	US-09-060-692-14	Sequence 14, Appl
41	16	80.0	5	2	US-08-833-391-14	Sequence 14, Appl
42	16	80.0	5	2	US-09-060-610-14	Sequence 14, Appl
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44	16	80.0	6	1	US-08-121-713D-16	Sequence 16, Appl
45	16	80.0	6	1	US-08-835-268-16	Sequence 16, Appl
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58	16	80.0	8	2	US-09-239-043D-999	Sequence 999, App
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61	16	80.0	8	2	US-09-435-945-9	Sequence 9, Appli
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73	16	80.0	9	2	US-09-510-738A-156	Sequence 156, App
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79	16	80.0	9	2	US-09-861-966-156	Sequence 156, App
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84	16	80.0	9	2	US-09-239-043D-1784	Sequence 1784, Ap
85	16	80.0	9	2	US-09-239-043D-2053	Sequence 2053, Ap
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91	16	80.0	9	2	US-09-919-048-156	Sequence 156, App
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135	15	75.0	8	2	US-08-477-778-1	Sequence 1, Appli
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140	15	75.0	9	1	US-08-178-570-18	Sequence 18, Appl
141	15	75.0	9	1	US-08-215-805A-41	Sequence 41, Appl
142	15	75.0	9	1	US-08-486-057B-32	Sequence 32, Appl
143	15	75.0	9	1	US-08-615-181-43	Sequence 43, Appl
144	15	75.0	9	1	US-08-789-588-32	Sequence 32, Appl
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146	15	75.0	9	2	US-08-159-339A-395	Sequence 395, App
147	15	75.0	9	2	US-08-842-079-12	Sequence 12, Appl
148	15	75.0	9	2	US-09-518-046-41	Sequence 41, Appl
149	15	75.0	9	2	US-09-518-046-94	Sequence 94, Appl
150	15	75.0	9	2	US-09-638-857-12	Sequence 12, Appl

ALIGNMENTS

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RESULT 1
US-08-403-459-43
; Sequence 43, Application US/08403459
; Patent No. 6514942
;  GENERAL INFORMATION:
;    APPLICANT:  Ioannides, Constantin G.
;    APPLICANT:  Fisk, Bryan A.
;    APPLICANT:  Ioannides, Maria G.
;    TITLE OF INVENTION:  METHODS AND COMPOSITIONS FOR STIMULATING
;    TITLE OF INVENTION:  T-LYMPHOCYTES
;    NUMBER OF SEQUENCES:  68
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Arnold, White & Durkee
;      STREET:  P.O. Box 4433
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  United States of America
;      ZIP:  77210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS/ASCII
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/403,459
;      FILING DATE:  Concurrently Herewith
;      CLASSIFICATION:  514
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;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kitchell, Barbara S.
;      REGISTRATION NUMBER:  33,928
;      REFERENCE/DOCKET NUMBER:  UTSC:390/KIT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (512) 418-3000
;      TELEFAX:  (713) 789-2679
;      TELEX:  79-0924
;  INFORMATION FOR SEQ ID NO:  43:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-403-459-43

  Query Match             100.0%;  Score 20;  DB 2;  Length 7;
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  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FREL 4
              ||||
Db          2 FREL 5



RESULT 36
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; Sequence 2, Application US/08685589A
; Patent No. 5916872
;  GENERAL INFORMATION:
;    APPLICANT:  Chang, Conway
;    APPLICANT:  Gu, Leo
;    APPLICANT:  Chen, Jie
;    TITLE OF INVENTION:  CYCLIC PEPTIDES HAVING BROAD
;    TITLE OF INVENTION:  SPECTRUM ANTIMICROBIAL ACTIVITY
;    NUMBER OF SEQUENCES:  222
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/685,589A
;      FILING DATE:  24-JUL-1996
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
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;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Coruzzi, Laura A.
;      REGISTRATION NUMBER:  30,742
;      REFERENCE/DOCKET NUMBER:  8067-026-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-790-9090
;      TELEFAX:  212-869-9741
;      TELEX:  66141
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  No. 5916872 Relevant
;    MOLECULE TYPE:  peptide
;    FEATURE:
;      NAME/KEY:  Peptide
;      LOCATION:  1..4
;      OTHER INFORMATION:  /product= "Beta-turn"
US-08-685-589A-2

  Query Match             80.0%;  Score 16;  DB 1;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 4.6e+05;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FRE 3
              |||
Db          2 FRE 4


Search completed: March  2, 2006, 12:36:31
Job time : 25 secs
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